

ADAPTIVE MEAN-SHIFT REGISTRATION OF WHITE MATTER TRACTOGRAPHIES

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ABSTRACT

In this paper we present a robust approach to the registration of white matter tractographies extracted from DT-MRI scans. The fibers are projected into a high dimensional feature space defined by the sequence of their 3D coordinates. Adaptive mean-shift (AMS) clustering is applied to extract a compact set of representative fiber-modes (FM). Each FM is assigned to a multivariate Gaussian distribution according to its population thereby leading to a Mixture of Gaussians (MoG) representation for the entire set of fibers. The registration between two fiber sets is treated as the alignment of two MoGs and is performed by maximizing their correlation ratio. A 9 parameter affine transform is recovered and eventually refined to a 12 parameters affine transform using an innovative mean-shift (MS) based registration refinement scheme presented in this paper. The validation of the algorithm on intra-subject data demonstrates its robustness against two main tractography artifacts: interrupted and deviating fiber tracts.

Index Terms— registration, Gaussian mixture model, white matter, tractography, mean-shift

1. INTRODUCTION

The increasing popularity of DT-MRI among brain researchers and clinicians has created the need for robust registration methods for white matter (WM) tractographies that allow for longitudinal (intra-subject) and population (inter-subjects) studies. Registration is performed at the tensor level before the tractographies are computed so that the same ROI can be used in the aligned brains [1, 2, 3]. In comparison to the scalar case, tensor registration involves much more data (6 numbers per voxel) and requires an additional step of tensor reorientation. An alternative is to perform registration between scalar images such as fractional anisotropy and then apply the recovered transform to the fibers. A joint clustering step of both tractography's fibers is then applied to obtain correspondences at clusters level [4].

Recently, methods have been proposed for direct registration between fiber sets [5, 6]. WM fibers, which consist of a sequence of connected 3D points, are more informative than the original tensor field and may therefore improve registration robustness. In [5], curvature and torsion features have

been used to describe each fiber in a multi-scale framework. A mean square difference is then used to measure similarity between fibers at different scale levels. Most similar fibers are matched and used to fit a global rigid transform. The method is based on rotation and translation invariance of the curvature and torsion features, therefore it is limited to rigid registration. In [6], the fibers are represented by their spatial coordinates sequences and considered as points in a high dimensional feature space. Affine Registration is then resolved by an efficient iterative closest feature point algorithm that tackles the computational bottleneck of high dimensional search by implementing approximate nearest neighbors techniques. As fiber-based registration methods rely on tractography results, they are naturally exposed to common tractography artifacts such as interrupted or deviating fiber tracts. These issues have not been addressed in previous fiber based registration algorithms.

In this work we propose an innovative tractography registration method that is robust to large amounts of interrupted and deviating fiber tracts. The main contributions of this work are: 1) Automated selection of a compact and reliable set of representative fibers by adaptive mean shift clustering. 2) Fiber registration is treated as the alignment of two continuous distributions. 3) The connectivity constraint for the points belonging to the same fiber as is naturally enforced by the feature space representation. 4) Innovative mean-shift based method to refine FMs positions thereby increasing registration accuracy.

The rest of this paper is organized as follows: In section 2 we describe the proposed algorithm. In section 3 we perform quantitative validation on intra-subject registration for various amounts of fiber interruptions and deviations. Conclusions and discussion are presented in section 4.

2. METHODS

The proposed registration algorithm consists of 5 main steps as described in the following subsections.

2.1. Preprocessing

The fibers generated by tractography softwares are represented by variable length sequences of 3D coordinates. Fibers

shorter than 10mm are removed since most of them correspond to artifacts located outside the brain. Each fiber is then re-sampled at 20 equally spaced points creating a constant length representation. The number of sampling points is an empirical compromise between dimensionality and fidelity to the original representation. The concatenation of the resulting (x,y,z) samples generates a 60×1 feature vector. Tractography softwares may produce one out of two flipped representations for each fiber. This may cause two spatially adjacent fibers to be distant in the feature space. In order to standardize fibers representation, the distance between each fiber ending points is calculated in each axis obtaining the triplet $d = \{d_x, d_y, d_z\}$, and the direction of maximum distance is extracted. The points sequence is flipped if this distance is negative.

2.2. Clustering using Adaptive Mean-shift

Once a uniform length representation for the fibers is achieved, it is necessary to find a more compact yet reliable description of the entire fiber set in order to reduce the amount of fibers. This goal is achieved by applying clustering separately to the model and target fiber sets to be registered.

In this work we use the adaptive mean-shift for fiber clustering. Each cluster is represented by a selected fiber hereafter termed fiber-mode (FM) as will be explained shortly. The FMs are equivalent to landmarks used in point based registration, which in our case are extracted automatically by the clustering. The adaptive Mean-Shift is an iterative procedure which estimates the local maxima, or modes, of the underlying density distribution for a given data set in a feature space [7].

Consider n vectors $\mathbf{x}_i \in \mathbb{R}^d$. To derive the mean-shift (MS) we begin with defining the *sample point* estimator at location \mathbf{x} :

$$\hat{f}_K(\mathbf{x}) = \frac{1}{n} \sum_{i=1}^n \frac{1}{h_i^d} k\left(\left\|\frac{\mathbf{x} - \mathbf{x}_i}{h_i}\right\|^2\right) \quad (1)$$

Where \mathbf{k} is the profile of the kernel \mathbf{K} such that

$$\mathbf{K}(x) = c_{d,k} k(\|x\|^2) > 0 \quad \|x\| \leq 1 \quad (2)$$

$c_{d,k}$ is a normalization factor and the bandwidth h_i defines the range of influence of the kernel centered at x_i . In this work, h_i is set to the distance between x_i and its p^{th} nearest neighbor. Taking the adaptive bandwidths leads to the AMS. Provided that the derivative of the profile \mathbf{k} exists, another profile $\mathbf{g}(x)$ and its kernel $\mathbf{G}(x)$ are defined:

$$g(x) = -k'(x) \quad \mathbf{G}(x) = c_{d,g} g(\|x\|^2) \quad (3)$$

It can be shown that by taking the gradient of Eq. 1, the following expression for the MS vector is obtained:

$$\mathbf{m}_G(x) = C \frac{\hat{\nabla} f_K(x)}{\hat{f}_G(x)} = \frac{\sum_{i=1}^n \frac{x_i}{h_i^{d+2}} g\left(\left\|\frac{x - x_i}{h_i}\right\|^2\right)}{\sum_{i=1}^n \frac{1}{h_i^{d+2}} g\left(\left\|\frac{x - x_i}{h_i}\right\|^2\right)} - x \quad (4)$$

Equation 4 shows that the mean shift vector is proportional to the normalized gradient of density estimate computed from kernel \mathbf{K} . Thus, the mean shift vector points at the direction of maximum density increase. Moreover, since the magnitude of the mean shift vector depends on the inverse of the density estimation using kernel \mathbf{G} , it gradually decreases as we move with the MS vector into high density region and eventually converge into a local maximum of density or a stationary point. MS clustering is obtained by starting from every data point and moving iteratively along the MS vector according to Eq. 5 until convergence [8].

$$y_{j+1} = \frac{\sum_{i=1}^n \frac{1}{h_i^{d+2}} x_i g\left(\left\|\frac{y_j - x_i}{h_i}\right\|^2\right)}{\sum_{i=1}^n \frac{1}{h_i^{d+2}} g\left(\left\|\frac{y_j - x_i}{h_i}\right\|^2\right)} \quad (5)$$

In the following we will refer to each convergence point as a FM. Usually the number of modes is much smaller than the original number of data points. It is important to note that the number of modes is an output of the MS algorithm and is not pre-set by the user. This is particularly useful for tractography data for which the number of similar fibers clusters may be difficult to set a-priori.

In Figure 1 we illustrate the results of the AMS clustering. Figure 1a shows the model fibers set which consists of about 95000 fibers. Figure 1b shows the 195 fiber modes obtained by applying the AMS algorithm on the full model fiber set. Figure 1c shows the 195 clusters represented by these FMs, each cluster is colored by a unique color. Figure 1d illustrates the correspondence between clusters and anatomical tracts by manually extracting 6 specific modes which represent the corticospinal tract.

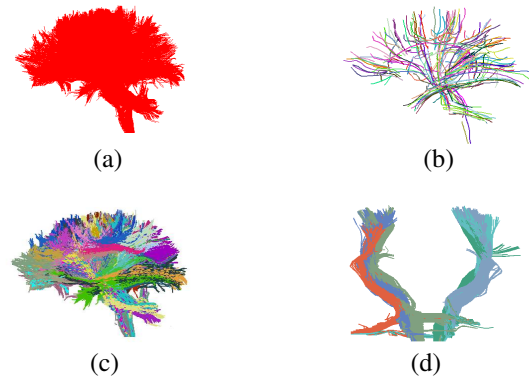


Fig. 1. (a) The original set (about 95000 fibers); (b) clustering into 195 FMs by the AMS; (c) the clustered fibers; (d) six specific modes representing the corticospinal tract

2.3. Gaussian mixture modeling

Following the clustering, we obtain model and target FM sets representing M and N clusters, respectively. Each FM represents a population of fibers, these populations are of different sizes and spatial distributions. In the following, we will treat registration as alignment to two MoGs [9]. For that purpose

we model each FM set by a MoG.

Each Gaussian is defined in 60-dimensional feature space, by assigning each FM with 3 parameters: *weight*, *mean* and *covariance matrix*, as follows: The *weight* is the ratio between the number of fibers assigned to the FM and the total number of fibers. The *mean* is the feature vector of the corresponding FM. The *covariance matrix* is defined to be $\lambda \mathbf{I}$ where \mathbf{I} is the identity matrix and λ a scalar constant. For each Gaussian, λ is defined to be the average variance of all the entries in the corresponding mean vector. The resulting MoGs have M and N components respectively.

2.4. Registration of MoGs

Once the MoGs representations are obtained, the task of registering two FM sets is shifted to registering their respective MoGs. Formally, consider two MoGs $f(x)$, $g(x)$ of size M and N respectively:

$$f(x) = \sum_{i=1}^M \alpha_i \Phi(x|\mu_i, \Sigma_i) \quad g(x) = \sum_{j=1}^N \beta_j \Phi(x|\nu_j, \Gamma_j) \quad (6)$$

where Φ denotes a 60-dimensional normal distribution. A 9 parameters affine transformation (rotation, translation and scaling in xyz axes) relating these MoGs can be parameterized by a non-singular block diagonal 60 x 60 matrix \mathbf{A} and a translation vector \mathbf{t} of size 60 x 1. Each block element along the diagonal of \mathbf{A} is the basic affine transformation matrix of size 3 x 3 built out of the 9 parameters which relates to a single point in 3D space. \mathbf{t} is simply the concatenation of the translation vector repetitively. In order to reorient the covariance matrices, \mathbf{A} is factorized using polar decomposition $\mathbf{A} = \mathbf{Q}\mathbf{S}$ which results in an orthogonal matrix \mathbf{Q} and a symmetric matrix \mathbf{S} [9]. Transforming $f(x)$ using the above mentioned transformation we get:

$$f_{A,t}(x) = \sum_{i=1}^M \alpha_i \Phi(x|A\mu_i + t, Q\Sigma_i Q^T) \quad (7)$$

We find the optimal transformation between these MoGs using a correlation based cost function. The correlation between two MoGs is given by the expression:

$$\sigma_{fg} = \int f g dx = \sum_{i=1}^M \sum_{j=1}^N \alpha_i \beta_j \int \Phi(x|\mu_i, \Sigma_i) \Phi(x|\nu_j, \Gamma_j) dx. \quad (8)$$

Using the formula

$$\int \Phi(x|\mu, \Sigma) \Phi(x|\nu, \Gamma) dx = \Phi(0|\mu - \nu, \Sigma + \Gamma) \quad (9)$$

we get

$$\sigma_{fg} = \sum_{i=1}^M \sum_{j=1}^N \alpha_i \beta_j \Phi(0|\mu_i - \nu_j, \Sigma_i + \Gamma_j). \quad (10)$$

The 9 parameters affine transformation relating these MoGs is found by maximizing the following correlation ratio:

$$E = \frac{\sigma_{fg}^2}{\sigma_f^2 \sigma_g^2}. \quad (11)$$

where σ_f^2 and σ_g^2 are the respective MoGs autocorrelations. The proposed cost function is differentiable, thus gradient based optimization methods such as the Quasi-Newton method can be used to maximize it.

2.5. Refinement of the registration

Using the estimated 9 parameters transform, the model modes are warped towards the target modes. Next we embed the warped model modes into the full target fibers set and run a MS procedure from each warped mode according to Eq. 5 where, in this case \mathbf{x}_i are the full target fibers set and \mathbf{y}_0 are the warped model modes. Assuming the warped modes are lying within the basin of attraction of their corresponding target modes, they will reach them during the MS procedure. This step generates a set of corresponding (non-warped) model and target modes from which we estimate a 12 parameters affine transform using a robust RANSAC scheme on the set of corresponding coordinates [10].

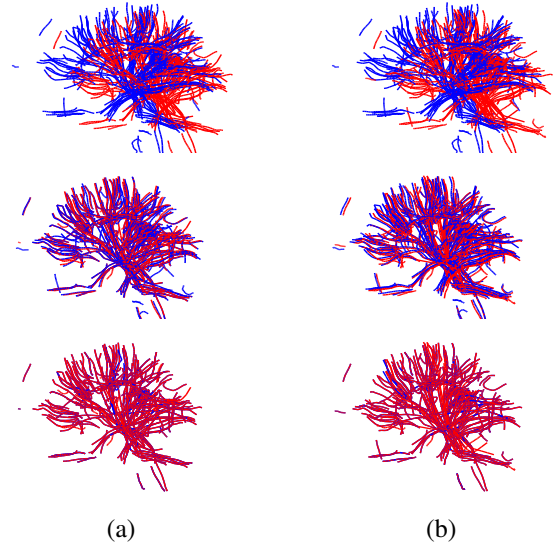


Fig. 2. Model and Target modes for fiber interruptions (a) and fiber deviations (b). First row - FM misaligned sets. Second row - FM sets after MoG registration. Third row - FM sets after registration refinement

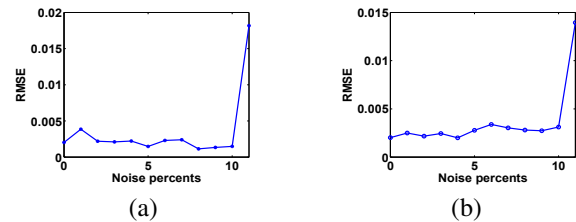


Fig. 3. RMSE results for various amounts of noisy fibers for (a) fiber splitting (b) fiber deviations.

3. EXPERIMENTAL RESULTS

In this section we present initial results for intra-subject DTI data. Tractographies were obtained from a real DTI brain¹ using DTIstudio [11]. Intra-subject data was simulated by applying a predefined 9 parameters affine transformation² on a set of tractographies. Two mechanisms were used to simulate the above mentioned tractographies artifacts. Fiber interruptions were simulated by splitting varying percents of randomly selected fibers at arbitrary points along the fibers. Fiber deviations were simulated by randomly selecting varying amounts of fibers, splitting them at arbitrary points creating two tails and reconnecting one of the tails to the nearest fiber tail within the entire fiber set. Only fiber extremities closer than 10mm are considered for reconnection. In order to preserve fibers smoothness, tails may only be reconnected when the resulting fiber turning angle is smaller than 70 degrees. In the following experiments, the model consists of the original fiber set. The target set is obtained by adding one of the noise artifacts to the transformed fibers set. The algorithm's accuracy is measured by calculating the root mean square error (RMSE) between the warped model and the target fiber sets. AMS clustering was applied to the model and target sets for $p = 200$. In Figure 2 we illustrate the registration results at different steps of the algorithm for 6% noise. Left and right columns refer to fiber interruptions and deviations, respectively. In the first row we show the initially misaligned model (blue) and target (red) FM sets. In second row we show the warped model (blue) and the target (red) FM sets after MoG registration. All the optimization procedures for MoG registrations are initialized using the identity transformation. The FM sets after registration refinement are shown in the third row. Results for the interrupted and deviated fibers are plotted in Figures 3a and 3b, respectively. The RMSE between the registered sets is plotted for different amounts of artifact noise. We observe robustness across a wide range of noise amounts for both types of artifacts. The RMSE is reduced by a factor of 20 for noise amounts up to 10% as the RMSE for the originally misaligned fiber sets is 0.043.

4. DISCUSSION

This paper proposed a method for direct registration of brain white matter fiber sets without requiring MRI or tensor registration. The main advantage of performing registration at fibers level rather than at voxels or tensors level is the connectivity information entailed in the fiber representation. The AMS clustering provides with a set anatomically consistent

FMs which significantly reduce the amount of data. Registration is based on modeling each of the FM sets using continuous MoGs and optimizing their correlation ratio. The continuous modeling enables the usage of gradient based optimization methods. The AMS based refinement procedure improves registration by handling local variations in modes positions due to noise. Our method demonstrated robustness to large amounts of tractography artifacts noise on a real brain from Johns Hopkins University data set¹. These results were confirmed on a second real brain³. We are currently gathering statistics on the entire 15 brains Johns Hopkins data set. In future work we shall further optimize the algorithm parameters and investigate their influence on registration results. Furthermore, we intend to apply the method to inter-subject data and extend it to non-linear transformations.

Acknowledgements

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5. REFERENCES

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¹DTI brain No. 6 downloaded from Johns Hopkins University medical MRI lab, 15 brains data set <http://lbam.med.jhmi.edu/>.

²Transformation parameters: $\{\theta_x = 8, \theta_y = 3, \theta_z = 12, t_x = 6, t_y = 15, t_z = -10, s_x = 1.1, s_y = 0.9, s_z = 1\}$ where θ_i denote the rotation angle around axis i , s_i denotes scaling factor in axis i and t_i denotes translation in axis i ($i = x, y, z$)

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